



PCT

## RAW SEQUENCE LISTING

DATE: 10/11/2005

PATENT APPLICATION: US/10/549,871

TIME: 11:35:45

Input Set : N:\Cr4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

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1 <110> APPLICANT: Kunkel, Andreas
2      Veen, Markus
3      Lang, Christine
4 <120> TITLE OF INVENTION: Method for producing ergosta-5,7-dienol and/or biosynthetic
5      intermediate and/or secondary products thereof in transgenic
6      organisms
7 <130> FILE REFERENCE: 12810-00126-US
8 <140> CURRENT APPLICATION NUMBER: US/10/549,871
9 <141> CURRENT FILING DATE: 2005-09-16
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002582
11 <151> PRIOR FILING DATE: 2004-03-12
12 <150> PRIOR APPLICATION NUMBER: DE 103 12 314.8
13 <151> PRIOR FILING DATE: 2003-03-19
14 <160> NUMBER OF SEQ ID NOS: 14
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1617
19 <212> TYPE: DNA
20 <213> ORGANISM: Saccharomyces cerevisiae
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22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(1617)
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27      1              5              10              15
28      acg cta cac caa ttg gct aaa gac cag ccc tct gta ggc gtc act act      96
29      Thr Leu His Gln Leu Ala Lys Asp Gln Pro Ser Val Gly Val Thr Thr
30      20              25              30
31      gcc ttc agt atc ctg gat aca ctt aag tct atg tca tat ttg aaa ata      144
32      Ala Phe Ser Ile Leu Asp Thr Leu Lys Ser Met Ser Tyr Leu Lys Ile
33      35              40              45
34      ttt gct act tta atc tgt att ctt ttg gtt tgg gac caa gtt gca tat      192
35      Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr
36      50              55              60
37      caa atc aag aaa ggt tcc atc gca ggt cca aag ttt aag ttc tgg ccc      240
38      Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro
39      65              70              75              80
40      atc atc ggt cca ttt ttg gaa tcc tta gat cca aag ttt gaa gaa tat      288
41      Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr
42      85              90              95
43      aag gct aag tgg gca tcc ggt cca ctt tca tgt gtt tct att ttc cat      336
44      Lys Ala Lys Trp Ala Ser Gly Pro Leu Ser Cys Val Ser Ile Phe His

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| 45 |     | 100 |     | 105 |     | 110 |     |     |
| 46 | aaa | ttt | ggt | ggt | atc | gca | tct | act |
| 47 | Lys | Phe | Val | Val | Ile | Ala | Ser | Thr |
| 48 |     | 115 |     | 120 |     | 125 |     |     |
| 49 | caa | tct | tcc | aaa | ttc | gtc | aaa | cct |
| 50 | Gln | Ser | Ser | Lys | Phe | Val | Lys | Pro |
| 51 |     | 130 |     | 135 |     | 140 |     |     |
| 52 | atc | tta | aga | cct | tgc | aat | tgg | ggt |
| 53 | Ile | Leu | Arg | Pro | Cys | Asn | Trp | Val |
| 54 |     | 145 |     | 150 |     | 155 |     | 160 |
| 55 | gat | tac | aga | aaa | tca | tta | aac | ggt |
| 56 | Asp | Tyr | Arg | Lys | Ser | Leu | Asn | Gly |
| 57 |     |     |     | 165 |     | 170 |     | 175 |
| 58 | caa | tac | tta | cct | tca | ttg | gaa | caa |
| 59 | Gln | Tyr | Leu | Pro | Ser | Leu | Glu | Gln |
| 60 |     | 180 |     | 185 |     | 190 |     |     |
| 61 | ttt | ggt | cgt | tta | tct | aag | gag | aat |
| 62 | Phe | Val | Arg | Leu | Ser | Lys | Glu | Asn |
| 63 |     | 195 |     | 200 |     | 205 |     |     |
| 64 | cat | gaa | atg | aga | gaa | att | ctt | tgc |
| 65 | His | Glu | Met | Arg | Glu | Ile | Leu | Cys |
| 66 |     | 210 |     | 215 |     | 220 |     |     |
| 67 | ggt | aac | tat | att | acc | gaa | gat | caa |
| 68 | Gly | Asn | Tyr | Ile | Thr | Glu | Asp | Gln |
| 69 |     | 225 |     | 230 |     | 235 |     | 240 |
| 70 | tat | ttg | ggt | aca | gca | gca | ttg | gaa |
| 71 | Tyr | Leu | Val | Thr | Ala | Ala | Leu | Glu |
| 72 |     |     |     | 245 |     | 250 |     | 255 |
| 73 | cct | tac | act | aaa | aca | tgg | tat | ggt |
| 74 | Pro | Tyr | Thr | Lys | Thr | Trp | Tyr | Gly |
| 75 |     |     |     | 260 |     | 265 |     | 270 |
| 76 | aag | att | ttc | gaa | aac | tgt | gct | caa |
| 77 | Lys | Ile | Phe | Glu | Asn | Cys | Ala | Gln |
| 78 |     | 275 |     | 280 |     | 285 |     |     |
| 79 | ggt | ggt | aag | cca | ggt | tgt | ggt | atg |
| 80 | Gly | Gly | Lys | Pro | Val | Cys | Val | Met |
| 81 |     | 290 |     | 295 |     | 300 |     |     |
| 82 | gat | gca | aag | aat | agt | aac | gat | gat |
| 83 | Asp | Ala | Lys | Asn | Ser | Asn | Asp | Asp |
| 84 |     | 305 |     | 310 |     | 315 |     | 320 |
| 85 | ttt | act | aac | aag | gaa | atc | tcc | gaa |
| 86 | Phe | Thr | Asn | Lys | Glu | Ile | Ser | Glu |
| 87 |     |     |     | 325 |     | 330 |     | 335 |
| 88 | tct | caa | gat | gcc | tct | tct | tct | tta |
| 89 | Ser | Gln | Asp | Ala | Ser | Ser | Ser | Leu |
| 90 |     |     |     | 340 |     | 345 |     | 350 |
| 91 | gct | gac | cgt | cca | gat | gtc | tta | gct |
| 92 | Ala | Asp | Arg | Pro | Asp | Val | Leu | Ala |
| 93 |     | 355 |     | 360 |     | 365 |     |     |

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Output Set: N:\CRF4\10062005\J549871.raw

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95      Val Arg Asn Asn Asp Met Ser Thr Glu Leu Asn Leu Asp Leu Ile Glu
96      370                      375                      380
97      aaa atg aag tac acc aat atg gtc ata aaa gaa act ttg cgt tac aga      1200
98      Lys Met Lys Tyr Thr Asn Met Val Ile Lys Glu Thr Leu Arg Tyr Arg
99      385                      390                      395                      400
100     cct cct gtc ttg atg gtt cca tat gtt gtt aag aag aat ttc cca gtt      1248
101     Pro Pro Val Leu Met Val Pro Tyr Val Val Lys Lys Asn Phe Pro Val
102     405                      410                      415
103     tcc cct aac tat acc gca cca aag ggc gct atg tta att cca acc tta      1296
104     Ser Pro Asn Tyr Thr Ala Pro Lys Gly Ala Met Leu Ile Pro Thr Leu
105     420                      425                      430
106     tac cca gct tta cat gat cct gaa gtt tac gaa aat cct gat gag ttc      1344
107     Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe
108     435                      440                      445
109     atc cct gaa aga tgg gta gaa ggc tct aag gct agt gaa gca aag aag      1392
110     Ile Pro Glu Arg Trp Val Glu Gly Ser Lys Ala Ser Glu Ala Lys Lys
111     450                      455                      460
112     aat tgg ttg gtt ttt ggt tgt ggt cca cac gtt tgc tta ggt caa aca      1440
113     Asn Trp Leu Val Phe Gly Cys Gly Pro His Val Cys Leu Gly Gln Thr
114     465                      470                      475                      480
115     tat gtc atg att acc ttc gcc gct ttg ttg ggt aaa ttt gca cta tat      1488
116     Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr
117     485                      490                      495
118     act gat ttc cat cat aca gtg act cca tta agt gaa aaa atc aag gtt      1536
119     Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val
120     500                      505                      510
121     ttc gct aca att ttc cca aaa gat gat ttg tta ctg act ttc aaa aag      1584
122     Phe Ala Thr Ile Phe Pro Lys Asp Asp Leu Leu Leu Thr Phe Lys Lys
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129 <211> LENGTH: 538
130 <212> TYPE: PRT
131 <213> ORGANISM: Saccharomyces cerevisiae
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135     Thr Leu His Gln Leu Ala Lys Asp Gln Pro Ser Val Gly Val Thr Thr
136     20                      25                      30
137     Ala Phe Ser Ile Leu Asp Thr Leu Lys Ser Met Ser Tyr Leu Lys Ile
138     35                      40                      45
139     Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr
140     50                      55                      60
141     Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro
142     65                      70                      75                      80
143     Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr

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| 144 |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| 145 | Lys | Ala | Lys | Trp | Ala | Ser | Gly | Pro | Leu | Ser | Cys | Val | Ser | Ile | Phe | His |
| 146 |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| 147 | Lys | Phe | Val | Val | Ile | Ala | Ser | Thr | Arg | Asp | Leu | Ala | Arg | Lys | Ile | Leu |
| 148 |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| 149 | Gln | Ser | Ser | Lys | Phe | Val | Lys | Pro | Cys | Val | Val | Asp | Val | Ala | Val | Lys |
| 150 |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| 151 | Ile | Leu | Arg | Pro | Cys | Asn | Trp | Val | Phe | Leu | Asp | Gly | Lys | Ala | His | Thr |
| 152 |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| 153 | Asp | Tyr | Arg | Lys | Ser | Leu | Asn | Gly | Leu | Phe | Thr | Lys | Gln | Ala | Leu | Ala |
| 154 |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |
| 155 | Gln | Tyr | Leu | Pro | Ser | Leu | Glu | Gln | Ile | Met | Asp | Lys | Tyr | Met | Asp | Lys |
| 156 |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| 157 | Phe | Val | Arg | Leu | Ser | Lys | Glu | Asn | Asn | Tyr | Glu | Pro | Gln | Val | Phe | Phe |
| 158 |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| 159 | His | Glu | Met | Arg | Glu | Ile | Leu | Cys | Ala | Leu | Ser | Leu | Asn | Ser | Phe | Cys |
| 160 |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| 161 | Gly | Asn | Tyr | Ile | Thr | Glu | Asp | Gln | Val | Arg | Lys | Ile | Ala | Asp | Asp | Tyr |
| 162 |     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| 163 | Tyr | Leu | Val | Thr | Ala | Ala | Leu | Glu | Leu | Val | Asn | Phe | Pro | Ile | Ile | Ile |
| 164 |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |
| 165 | Pro | Tyr | Thr | Lys | Thr | Trp | Tyr | Gly | Lys | Lys | Thr | Ala | Asp | Met | Ala | Met |
| 166 |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| 167 | Lys | Ile | Phe | Glu | Asn | Cys | Ala | Gln | Met | Ala | Lys | Asp | His | Ile | Ala | Ala |
| 168 |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| 169 | Gly | Gly | Lys | Pro | Val | Cys | Val | Met | Asp | Ala | Trp | Cys | Lys | Leu | Met | His |
| 170 |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| 171 | Asp | Ala | Lys | Asn | Ser | Asn | Asp | Asp | Asp | Ser | Arg | Ile | Tyr | His | Arg | Glu |
| 172 |     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| 173 | Phe | Thr | Asn | Lys | Glu | Ile | Ser | Glu | Ala | Val | Phe | Thr | Phe | Leu | Phe | Ala |
| 174 |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     | 335 |
| 175 | Ser | Gln | Asp | Ala | Ser | Ser | Ser | Leu | Ala | Cys | Trp | Leu | Phe | Gln | Ile | Val |
| 176 |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| 177 | Ala | Asp | Arg | Pro | Asp | Val | Leu | Ala | Lys | Ile | Arg | Glu | Glu | Gln | Leu | Ala |
| 178 |     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| 179 | Val | Arg | Asn | Asn | Asp | Met | Ser | Thr | Glu | Leu | Asn | Leu | Asp | Leu | Ile | Glu |
| 180 |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| 181 | Lys | Met | Lys | Tyr | Thr | Asn | Met | Val | Ile | Lys | Glu | Thr | Leu | Arg | Tyr | Arg |
| 182 |     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| 183 | Pro | Pro | Val | Leu | Met | Val | Pro | Tyr | Val | Val | Lys | Lys | Asn | Phe | Pro | Val |
| 184 |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     |     | 415 |
| 185 | Ser | Pro | Asn | Tyr | Thr | Ala | Pro | Lys | Gly | Ala | Met | Leu | Ile | Pro | Thr | Leu |
| 186 |     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| 187 | Tyr | Pro | Ala | Leu | His | Asp | Pro | Glu | Val | Tyr | Glu | Asn | Pro | Asp | Glu | Phe |
| 188 |     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| 189 | Ile | Pro | Glu | Arg | Trp | Val | Glu | Gly | Ser | Lys | Ala | Ser | Glu | Ala | Lys | Lys |
| 190 |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| 191 | Asn | Trp | Leu | Val | Phe | Gly | Cys | Gly | Pro | His | Val | Cys | Leu | Gly | Gln | Thr |
| 192 |     | 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |

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Input Set : N:\Cr4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

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193   Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr
194               485                      490                      495
195   Thr Asp Phe His His Thr Val Thr Pro Leu Ser Glu Lys Ile Lys Val
196               500                      505                      510
197   Phe Ala Thr Ile Phe Pro Lys Asp Asp Leu Leu Leu Thr Phe Lys Lys
198               515                      520                      525
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200               530                      535
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203 <211> LENGTH: 1578
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial sequence
206 <220> FEATURE:
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208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature
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211 <223> OTHER INFORMATION: CDS
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214   Met Asp Gln Leu Val Lys Thr Glu Val Thr Lys Lys Ser Phe Thr Ala
215   1               5                      10                      15
216   cct gta caa aag gct tct aca cca gtt tta acc aat aaa aca gtc att      96
217   Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr Val Ile
218               20                      25                      30
219   tct gga tcg aaa gtc aaa agt tta tca tct gcg caa tcg agc tca tca      144
220   Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser
221               35                      40                      45
222   gga cct tca tca tct agt gag gaa gat gat tcc cgc gat att gaa agc      192
223   Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser
224               50                      55                      60
225   ttg gat aag aaa ata cgt cct tta gaa gaa tta gaa gca tta tta agt      240
226   Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu Leu Ser
227   65               70                      75                      80
228   agt gga aat aca aaa caa ttg aag aac aaa gag gtc gct gcc ttg gtt      288
229   Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala Leu Val
230               85                      90                      95
231   att cac ggt aag tta cct ttg tac gct ttg gag aaa aaa tta ggt gat      336
232   Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp
233               100                      105                      110
234   act acg aga gcg gtt gcg gta cgt agg aag gct ctt tca att ttg gca      384
235   Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala
236               115                      120                      125
237   gaa gct cct gta tta gca tct gat cgt tta cca tat aaa aat tat gac      432
238   Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr Asp
239               130                      135                      140
240   tac gac cgc gta ttt ggc gct tgt tgt gaa aat gtt ata ggt tac atg      480
241   Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met
242   145               150                      155                      160

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 10/11/2005

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TIME: 11:35:46

Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/549,871

DATE: 10/11/2005

TIME: 11:35:46

Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

**STATISTICS SUMMARY**

PATENT APPLICATION: US/10/549,871

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Input Set : N:\Crf4\10042005\J459871.raw

Output Set: N:\CRF4\10062005\J549871.raw

Application Serial Number: US/10/549,871

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 09-16-2005

Art Unit: PCT

Software Application: PatentIN3.3

Total Number of Sequences: 14

Total Nucleotides: 7803

Total Amino Acids: 2533

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 0

**MESSAGE SUMMARY**